

8/28
02/17/99

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/087,136DATE: 01/29/1999
TIME: 15:47:41

Input Set: I087136.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>

see R5

ENTERED

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1  <110> APPLICANT: H. Robert Horvitz
2  <120> TITLE OF INVENTION: A TUMOR SUPPRESSOR PATHWAY IN C. ELEGANS
3  <130> FILE REFERENCE: 01997/202002
4  <140> CURRENT APPLICATION NUMBER: US/09/087,136
5  <141> CURRENT FILING DATE: 1998-05-28
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7  <151> EARLIER FILING DATE: 1997-05-28
8  <160> NUMBER OF SEQ ID NOS: 16
9  <170> SOFTWARE: FastSEQ for Windows Version 3.0
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11 <211> LENGTH: 275
12 <212> TYPE: PRT
13 <213> ORGANISM: Caenorhabditis elegans
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18             20             25             30
19     Pro Leu Glu Ser Pro Ser Arg Lys Leu Thr Ser Leu Leu Ser Tyr Asp
20             35             40             45
21     Pro Thr Val Pro Glu Ser Pro Asp Met Lys Phe Ala Arg Lys Arg Leu
22             50             55             60
23     Gly Asn Leu Leu Thr Thr Ile Lys His His Pro Ser Glu Ile Ile Gly
24             65             70             75             80
25     Val Leu Pro Glu Asp Tyr Thr Arg Ala Asp Glu Glu Pro Gly Arg Gln
26             85             90             95
27     Gly Arg Pro Pro Gly Arg Pro Arg Lys Met Pro Arg His Glu Ser Ser
28             100            105            110
29     Thr Ser Leu Met Glu Ser Pro Arg Lys Thr Met Thr Arg Asp Ser Lys
30             115            120            125
31     Ile Met Phe Glu Leu Arg Gly Lys Pro Phe Glu Met Ile Ala Gly Arg
32             130            135            140
33     Phe Glu Glu Glu Tyr Ser Leu Gly Arg Ala Trp Val Lys Gly His Met
34             145            150            155            160
35     Asn Asn Glu Tyr Glu Pro Ile Lys Ala Gln Arg Thr Asp Tyr Ala Pro
36             165            170            175
37     Asn Leu Ala Val Asp Tyr Leu Ala Cys Arg Glu Ile His Arg Met Pro
38             180            185            190
39     Arg Pro Asp Lys Ser Ile Pro Glu Leu Pro Ile Val Pro Ser Arg Ile
40             195            200            205
41     Asp Glu Phe Asp Ala Thr Val Asp Pro Arg Tyr Glu Thr Asp Leu Lys
42             210            215            220
43     Asn Glu Tyr Ile Arg His Trp Lys Gln Val Lys Lys Gly Trp Cys Ala
44             225            230            235            240

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45      His Gln Arg Arg Arg Thr Ala Pro His Ala Arg Ser Ile Ala Leu Ile
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48                      260                      265                      270
49      Gly Leu Ile
50                      275
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53 <212> TYPE: DNA
54 <213> ORGANISM: Caenorhabditis elegans
55 <400> SEQUENCE: 2
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57      cgtcaaaatg atccattgat aagcggaggt ccacttccat tggaatcgcc aagcagaaaa      120
58      ctcacatccc tgttatccta tgatccgaca gttccggagt caccggatat gaaattcgcc      180
59      agaaaacgtc tgggaaatct gctgacaacc ataaaacatc acccatcgga aataattgga      240
60      gtactcccag aagattatac tcgtgctgat gaagagcccg ggcgcccaagg acgtccacca      300
61      ggtcgccctc gtaagatgcc gcgtcacgaa tcttcaactt cacttatgga atcaccacgc      360
62      aagactatga ctctgtattc taaaattatg tttgaattgc gtggaaaacc attcgaaatg      420
63      atagctggac gttttgaaga agaattattca cttggtagag catgggttaa aggacacatg      480
64      aataatgaat atgaaccaat aaaagctcaa aggacagact atgcaccgaa tctggctggt      540
65      gattatcttg catgtcgcga gattcatcga atgccacgtc cagataaatc aattcctgag      600
66      ctgccaatg ttccatctag aatcgatgaa ttcgacgcta cagtcgatcc aagatatgaa      660
67      acagatttga aaaatgaata cattcgtcat tggaaaacaag tcaaaaaagg ttggtgtgct      720
68      catcaacgtc gtcggactgc tccccatgca agaagcatag cattaatcaa caaaatctac      780
69      cagcctggag agtcgaaaac tgtcgagcaa gcacttggtc ttatttaaatt attctaacat      840
70      gtaatttcaa tttatctctt actttctgat cttgctatca catgtctctt atttcaaaaa      900
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74 <212> TYPE: PRT
75 <213> ORGANISM: Caenorhabditis elegans
76 <400> SEQUENCE: 3
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80                      20                      25                      30
81      Thr Asp Thr Ile Cys Glu Glu Pro Pro Ala Lys Arg Ile Asp Leu Asp
82                      35                      40                      45
83      Ile Lys Gln Glu Phe Asn Gly Gly Val Gln Ser Gly Gly Leu Ile Lys
84                      50                      55                      60
85      Asn Glu Ser Glu Leu Thr Gln Met Thr Ile Lys Gln Glu Thr Glu Gly
86      65                      70                      75                      80
87      Asn Ile Asn Glu Ala Arg Arg Glu Glu Glu Asp Glu Glu Gln Asp Glu
88                      85                      90                      95
89      Asp Ser Arg Thr Ser Met Pro Pro Ala Leu Gly Glu Asp Asp Asp Tyr
90                      100                      105                      110
91      Glu Glu Asp Asp Ala Asp Ser Phe Ile Asp Lys Thr Asn Thr Pro Pro
92                      115                      120                      125
93      Pro Ser Gln Ser Phe Leu Glu Gly Cys Arg Ala Ala Asn Leu Pro Asn
94                      130                      135                      140

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97	Val	Ser	Leu	Glu	Gly	Ser	Glu	Ser	Ala	Trp	Gln	Leu	Ser	Ala	Ile	Tyr
98					165					170						175
99	Tyr	Tyr	Leu	Leu	Ser	Lys	Gly	Ile	Lys	Arg	Arg	Gly	Lys	Thr	Ile	Arg
100					180					185					190	
101	Ile	Leu	Ile	Gln	Pro	Phe	Pro	Val	Ser	Ile	Leu	Thr	Ile	Ala	Asn	Ser
102					195					200				205		
103	Phe	Asp	Ile	Ser	Val	Ala	Glu	Met	Leu	Asp	Lys	Thr	Ala	Arg	Phe	Val
104		210						215					220			
105	Glu	Ile	Ile	His	Ser	Arg	Lys	Ile	Arg	Arg	Tyr	Gln	Glu	Tyr	Ile	Arg
106	225					230					235					240
107	Arg	Ile	Gln	Glu	Gly	Leu	Ala	Val	Ser	Cys	Val	Ile	Phe	Lys	Lys	Phe
108					245					250						255
109	Cys	Arg	Ile	Phe	Cys	Lys	Ile	Phe	Glu	Glu	Ile	Lys	Val	Gly	Ser	Glu
110					260					265					270	
111	Asn	Cys	Pro	Ser	Ser	His	Glu	Leu	Phe	Thr	Val	Leu	Trp	Thr	Ser	Phe
112					275					280				285		
113	Leu	Val	Met	Lys	Ser	Arg	Met	Thr	Val	Asp	Asp	Leu	Ile	Ser	Asn	Tyr
114		290						295					300			
115	Gln	Leu	Leu	Phe	Ser	Ile	Leu	Asp	Gln	Val	Tyr	Thr	Glu	Met	Cys	Ser
116	305					310					315					320
117	Met	Lys	Glu	Gly	Ile	Val	His	His	Leu	Asn	Gln	Lys	Phe	Val	Glu	Asp
118					325					330						335
119	Leu	Leu	Glu	Asn	Asp	Cys	Thr	Ile	Ile	Arg	Ala	Leu	Cys	Thr	Gln	Phe
120					340					345					350	
121	Gly	Gly	Ser	Val	Leu	Asp	Ala	Arg	His	Phe	Ser	Asp	His	Thr	Phe	Lys
122					355					360				365		
123	Lys	Met	Glu	Lys	Thr	Gly	Ile	Pro	Ser	Thr	Trp	Asn	Phe	Gln	Glu	Phe
124		370						375					380			
125	Arg	Asp	Leu	Ile	Met	Asn	Val	Pro	Lys	Thr	Ala	Tyr	Glu	Asn	Tyr	Leu
126	385					390					395					400
127	Leu	Gln	Arg	Gly	Ser	Ile	Asp	Glu	Arg	Ile	Phe	Ile	Pro	Ser	Val	Glu
128					405					410						415
129	Asp	Phe	Ser	Lys	Ile	Phe	Gln	Ser	Pro	Asp	Thr	Tyr	Ser	Val	Ala	Asp
130					420					425				430		
131	Ile	Leu	Lys	Val	Ser	Tyr	Ser	Gly	Arg	Arg	Phe	Arg	Asp	Ala	Glu	Phe
132					435				440					445		
133	Leu	Thr	Lys	Ile	Ser	Asn	Asn	His	Cys	Leu	Glu	Lys	Leu	Ala	Leu	Gly
134		450						455						460		
135	Gly	Lys	Val	Ala	Ser	Glu	Lys	Leu	Val	Thr	Gln	Ser	Lys	Glu	Gln	Pro
136	465					470					475					480
137	Arg	Val	Pro	Cys	Val	Glu	Tyr	Asn	Leu	Glu	Leu	Gly	Asn	Tyr	Pro	Asp
138					485					490						495
139	Asp	Leu	Glu	Ser	Asn	Asn	Gln	Ser	Leu	Tyr	Asn	Arg	Leu	Thr	Lys	Ile
140					500					505				510		
141	Ile	Gly	Ser	Trp	Lys	Leu	Glu	Asn	Ser	Lys	Leu	Glu	Glu	Val	Cys	Gly
142					515					520				525		
143	Thr	Met	Ser	Asp	Ser	Pro	Met	Ala	Thr	Ile	Leu	Leu	Lys	Ser	Asp	Glu
144					530					535				540		

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149	Glu Leu Val Phe Leu Ile Phe Met Glu Lys Ile Ile Val Ala Glu Leu
150	580 585 590
151	Lys Lys Lys Val Arg Glu Glu Asp Leu Leu Asn Val Ile Arg Arg Glu
152	595 600 605
153	Glu Phe Leu Asp Ser Val Phe Cys Phe Cys Val Glu Leu Ile Leu Val
154	610 615 620
155	Ser Asn Gly Tyr Asp Arg Pro Phe Pro Trp Ser Ala Glu Leu Cys Gly
156	625 630 635 640
157	Val His Pro Phe Met Phe His Lys Val Ile Asp Leu Met Ile Thr His
158	645 650 655
159	Glu Lys Gln Leu Ser Arg Gln Met Val Gln His Phe Ser Arg Ile Glu
160	660 665 670
161	Glu Thr Val Ile Glu Tyr Phe Ser Trp Lys Ser Asp Ser Pro Leu Trp
162	675 680 685
163	Pro Met Val Val Arg Cys Pro Phe Ala His Phe Gln Glu Phe Gly Glu
164	690 695 700
165	Asp Trp Ala Asp Lys Leu Asn Ser Tyr Ser Pro Ile Lys Phe Thr Pro
166	705 710 715 720
167	Ile Lys Lys Pro Asp Asp Leu Arg Asp Glu Leu Gly Arg Pro Ile Val
168	725 730 735
169	Pro Gln Asn Gln Thr Ser Arg Thr Leu Arg Ile Phe Leu Lys Arg Thr
170	740 745 750
171	Tyr Phe Thr Ala Ala Arg Arg Leu Gln Asp Leu Thr Asp Arg Val Ser
172	755 760 765
173	Met Gly Ala Arg Ala Lys Ser Gln Cys Trp Ser Leu Phe Asp Tyr Leu
174	770 775 780
175	Leu Arg Asn Asp Thr Leu Ile Phe Met Asp Arg His Leu Asp Gln Ile
176	785 790 795 800
177	Leu Leu Cys Cys Val Phe Val Ile Met Lys Ile Asn Glu Ser Ser Met
178	805 810 815
179	Leu Phe Thr Glu Ile Met Ala Gln Tyr Arg Arg Gln Ser Ala Asn Ser
180	820 825 830
181	Leu Leu Val Tyr Arg Ser Val Thr Val Phe Gln Glu Gln Leu Asn Pro
182	835 840 845
183	Glu Asn Pro Gln Ala Val Asn Thr Lys Glu Thr Ile Leu Glu Arg Leu
184	850 855 860
185	Glu Gly Pro Gln Lys Glu Lys Thr Thr Val Asp Ile Ile Lys Tyr Tyr
186	865 870 875 880
187	Asn Ile Glu Phe Arg Asp Arg Ile Lys Tyr Ile Ile Gly Gln Ile Asp
188	885 890 895
189	Ser Ala Ser Asp Glu Asp Leu Met Glu Met Pro Val Ala Thr Glu Ser
190	900 905 910
191	Gly Leu Met Pro Val Arg Val Tyr Leu Thr His Lys Leu Ser Ile Gln
192	915 920 925
193	Thr Leu Pro Lys Thr Lys His Gly Glu Ser Lys Gln Glu Arg Ala Ile
194	930 935 940

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205      ccagcaaaac gaatcgactt agatataaag caagaattca atggtggagt gcaaagtgga      180
206      gggctgatta aaaatgaatc cgaattgact caaatgacaa tcaaacaaga aacagaagga      240
207      aacataaatg aagctagacg agaagaagaa gacgaagaac aagatgaaga ttccagaaca      300
208      tcaatgccac ctgcattggg agaagatgat gattatgagg aggatgatgc tgatagtttt      360
209      attgataaaa ctaatacacc gccaccatca caatcatttc tgggaaggatg tcgagcagct      420
210      aattttacca atgacattgt tactggtgca tgggaaacgt acaaccacgc ggttcaacgg      480
211      gtttctcttg agggttcgga atcggcgtgg caactatcag caatttacta ttatcttcta      540
212      tcaaaaaggaa taaaacgtcg tggaaaaaca atccgtattc tcattcaacc gtttctgttt      600
213      tcgatactta caattgccaa ctcatcttgac atatccgttg ctgaaatgct tgacaaaact      660
214      gctcgatttg tggaaattat acattccaga aaaattcgtc gttatcaaga atatattcga      720
215      cgaattcaag aaggactcgc agtttcttgt gtgatattca aaaagttttg ccgaattttc      780
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217      tttacggttc tttggacatc ttttctggtg atgaaaagtc gaatgacagt ggacgatttg      900
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221      cacttttctg atcatacttt taagaaaatg gagaagactg gaattccgtc cacttggaaat      1140
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238      gaattcggag aggattgggc tgataaatta aactcgtact caccaataaa attcactcca      2160
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242      ttcgattatc ttcttcgcaa tgacactttg atttttatgg atagacatct tgatcaaatt      2400
243      cttctttgtt gcgtgtttgt cattatgaag ataaatgagt catcaatgct tttcacggaa      2460
244      ataatggctc aatatcgacg acaatcagcc aattctttgc tggctctaccg aagtgttaca      2520

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Please Note:

Use n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I087136.RAW

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724	W	"N" or "Xaa" used: Feature required	gaaaatcaaa ggcagcagcg gaacggatga tacttgag
725	W	"N" or "Xaa" used: Feature required	ntgtcatcaa ctctgcagga aaggcaaaaa ntgaccct
729	W	"N" or "Xaa" used: Feature required	taaatctgct tatgccctt ctaaattgaa tttttctn
740	W	"N" or "Xaa" used: Feature required	atttggcatg ggtggagaaa caaagnatcg ggaagctg